

SFQ ID NO.1FIG.1 a

GAATTCCCCCAACAGAGCCAAGCTCTCCATCTAGTGGACAGGGAAGCTAGCAGCAAACC
 TTCCCTTCACTACAAAACCTTCATTGCTTGGCCAAAAAGAGAGTTAATTCAATGTAGACAT
 CTATGTAGGCAATTAAAAACCTATTGATGTATAAAACAGTTTGCATTCATGGAGGGCAAC
 TAAATACATTCTAGGACTTTATAAAAGATCACTTTTTATTATGCACAGGGTGAACAAG
 ATGGATTATCAAGTGTCAAGTCCAATCTATGACATCAATTATTATACATCGGAGCCCTGC
 M D Y Q V S S P I Y D I N Y Y T S E P C
 CAAAAATCAATGTGAAGCAAATCGCAGCCCGCCTCCTGCCTCCGCTCTACTCACTGGTG
 Q K I N V K Q I A A R L L P P L Y S L V
 TTCATCTTTGGTTTTGTGGGCAACATGCTGGTCATCCTCATCCTGATAAACTGCAAAAGG
 I F G F V G N M L V I L I L I N C K R
 CTGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTTCCTT
 K S M T D I Y L L N L A I S D L F F L
 CTTACTGTCCCCTTCTGGGCTCACTATGCTGCCGCCAGTGGGACTTTGGAAATACAATG
 T V P F W A H Y A A A Q W D F G N T M
 TGTCAACTCTTGACAGGGCTCTATTTTATAGGCTTCTTCTCTGGAATCTTCTTCATCATC
 Q L L T G L Y F I G F F S G I F F I I
 CTCCTGACAATCGATAGGTACCTGGCTGTCGTCCATGCTGTGTTTGCTTTAAAAGCCAGG
 L L T I D R Y L A V V H A V F A L K A R
 ACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACTTGGGTGGTGGCTGTGTTTGCCTCT
 T V T F G V V T S V I T W V V A V F A S
 CTCCCAGGAATCATCTTTACCAGATCTCAAAAAGAAGGTCTTCATTACACCTGCAGCTCT
 L P G I I F T R S Q K E G L H Y T C S S
 CATTTTCCATACA
 H F P Y

59(UPPER:SEA ID) NO1
 19(LOWER:SEA ID) NO4

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GAATTCCCCCAACAGAGCCAAGCTCTCCATCTAGTGGACAGGGAAGCTAGCAGCAAACC 59(UPPER:SER L) NO2
 19(LOWER:SER L) NO5

TTCCCTTCACTACAAAACCTTCATTGCTTGGCCAAAAAGAGAGTTAATTCAATGTAGACAT 119
 39

CTATGTAGGCAATTAAAAACCTATTGATGTATAAAACAGTTTGCATTTCATGGAGGGCAAC 179
 59

TAAATACATTCTAGGACTTTATAAAAGATCACTTTTTTATTTATGCACAGGGTGAACAAG 239
 79

ATGGATTATCAAGTGTCAAGTCCAATCTATGACATCAATTATTATACATCGGAGCCCTGC 299
 M D Y Q V S S P I Y D I N Y Y T S E P C 99

CAAAAAATCAATGTGAAGCAAATCGCAGCCCGCCTCCTGCCTCCGCTCTACTCACTGGTG 359
 K I N V K Q I A A R L L P P L Y S L V 119

TCATCTTTGGTTTTGTGGGCAACATGCTGGTCACTCCTCATCTGATAAACTGCAAAGG 419
 I F G F V G N M L V I L I L I N C K R 139

GTGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTTCCTT 479
 L K S M T D I Y L L N L A I S D L F F L 159

GTACTGTCCCCTTCTGGGCTCACTATGCTGCCGCCAGTGGGACTTTGGAAATACAATG 539
 L T V P F W A H Y A A A Q W D F G N T M 179

EGTCAACTCTTGACAGGGCTCTATTTTATAGGCTTCTTCTGGAATCTTCTTCATCATC 599
 C Q L L T G L Y F I G F F S G I F F I I 199

CTCCTGACAATCGATAGGTACCTGGCTGTCGTCCATGCTGTGTTTGCTTTAAAGCCAGG 659
 L L T I D R Y L A V V H A V F A L K A R 219

ACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACTTGGGTGGTGGCTGTGTTTGCCTCT 719
 T V T F G V V T S V I T W V V A V F A S 239

CTCCAGGAATCATCTTTACCAGATCTCAAAAAGAAGGTCTTCATTACACCTGCAGCTCT 779
 L P G I I F T R S Q K E G L H Y T C S S 259

CATTTTCCATACAGTCAGTATCAATTCTGGAAGAATTTCCAGACATTAAAGATAGTCATC 839
 H F P Y S Q Y Q F W K N F Q T L K I V I 279

TTGGGGCTGGTCCTGCCGCTGCTTGTTCATGGTCATCTGCTACTCGGGAATCCTAAAAACT	899
L G L V L P L L V M V I C Y S G I L K T	299
CTGCTTCGGTGTCGAAATGAGAAGAAGAGGCACAGGGCTGTGAGGCTTATCTTCACCATC	959
L L R C R N E K K R H R A V R L I F T I	319
ATGATTGTTTATTTTCTCTTCTGGGCTCCCTACAACATTGTCCTTCTCCTGAACACCTTC	1019
M I V Y F L F W A P Y N I V L L L N T F	339
CAGGAATTCTTTGGCCTGAATAATTGCAGTAGCTCTAACAGGTTGGACCAAGCTATGCAG	1079
Q E F F G L N N C S S S N R L D Q A M Q	359
GTGACAGAGACTCTTGGGATGACGCACTGCTGCATCAACCCCATCATCTATGCCTTTGTC	1139
V T E T L G M T H C C I N P I I Y A F V	379
GGGGAGAAGTTTCAGAACTACCTCTTAGTCTTCTTCCAAAAGCACATTGCCAAACGCTTC	1199
G E K F R N Y L L V F F Q K H I A K R F	399
TGCAAATGCTGTTCTATTTTCCAGCAAGAGGCTCCCGAGCGAGCAAGCTCAGTTTACACC	1259
C K C C S I F Q Q E A P E R A S S V Y T	419
CGATCCACTGGGGAGCAGGAAATATCTGTGGGCTTGTGACACGGACTCAAGTGGGCTGGT	1319
R S T G E Q E I S V G L *	439
GACCCAGTCAGAGTTGTGCACATGGCTTAGTTTTTCATACACAGCCTGGGCTGGGGGTNGG	1379
	459
TGGNNGAGGTCTTTTTTAAAAGGAAGTTACTGTTATAGAGGGTCTAAGATTCATCCATT	1439
	479
TTTTGGCATCTGTTTAAAGTAGATTAGATCCGAATTC	

SEQ ID NO.2 (SUITE)

FIG.1c

GAATTCCCCCAACAGAGCCAAGCTCTCCATCTAGTGGACAGGGAAGCTAGCAGCAAACC
 TTCCCTTCACTACAAAACCTTCATTGCTTGGCCAAAAAGAGAGTTAATTCAATGTAGACAT
 CTATGTAGGCAATTAAAAACCTATTGATGTATAAAACAGTTTGCATTCATGGAGGGCAAC
 TAAATACATTCTAGGACTTTATAAAAGATCACTTTTTATTATGCACAGGGTGGAACAAG
 ATGGATTATCAAGTGTCAAGTCCAATCTATGACATCAATTATTATACATCGGAGCCCTGC
 M D Y Q V S S P I Y D I N Y Y T S E P C
 CAAAAATCAATGTGAAGCAAATCGCAGCCCGCCTCCTGCCTCCGCTCTACTCACTGGTG
 Q K I N V K Q I A A R L L P P L Y S L V
 TCATCTTTGGTTTTGTGGGCAACATGCTGGTCACTCCTCATCCTGATAAACTGCAAAGG
 F I F G F V G N M L V I L I L I N C K R
 GTGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTCTCT
 L K S M T D I Y L L N L A I S D L F F L
 TTTACTGTCCCCTTCTGGGCTCACTATGCTGCCGCCAGTGGGACTTTGGAAATACAATG
 L T V P F W A H Y A A A Q W D F G N T M
 TGTCAACTCTTGACAGGGCTCTATTTTATAGGCTTCTTCTCTGGAATCTTCTTCATCATC
 C Q L L T G L Y F I G F F S G I F F I I
 CTCCTGACAATCGATAGGTACCTGGCTGTGCTCCATGCTGTGTTTGCTTTAAAAGCCAGG
 L L T I D R Y L A V V H A V F A L K A R
 ACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACTTGGGTGGTGGCTGTGTTTGCGTCT
 T V T F G V V T S V I T W V V A V F A S
 CTCCCAGGAATCATCTTTACCAGATCTCAAAAAGAAGGTCTTCATTACACCTGCAGCTCT
 L P G I I F T R S Q K E G L H Y T C S S
 CATTTTCCATACATTAAAGATAGTCATCTTGGGGCTGGTCCGCTGCTTGTGTCATGGT
 H F P Y I K D S H L G A G P A A A C H G

59UPPER:SEQ ID NO.3
 19LOWER:SEQ ID NO.6

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SEQ ID NO.3

FIG.1d

CATCTGCTACTCGGGAATCCTAAAACTCTGCTTCGGTGTGCGAAATGAGAAGAAGAGGCA	899
H L L L G N P K N S A S V S K *	299
CAGGGCTGTGAGGCTTATCTTCACCATCATGATTGTTTATTTTCTCTTCTGGGCTCCCTA	959
	319
CAACATTGTCCTTCTCCTGAACACCTTCCAGGAATTCTTTGGCCTGAATAATTGCAGTAG	1019
	339
CTCTAACAGGTTGGACCAAGCTATGCAGGTGACAGAGACTCTTGGGATGACGCACTGCTG	1079
	359
CATCAACCCCATCATCTATGCCTTTGTGCGGGAGAAGTTCAGAACTACCTCTTAGTCTT	1139
	379
CTTCCAAAAGCACATTGCCAAACGCTTCTGCAAATGCTGTTCTATTTTCCAGCAAGAGGC	1199
	399
TCCCGAGCGAGCAAGCTCAGTTTACACCCGATCCACTGGGGAGCAGGAAATATCTGTGGG	1259
	419
CTGTGACACGGACTCAAGTGGGCTGGTGACCCAGTCAGAGTTGTGCACATGGCTTAGTT	1319
	439
TTATACACAGCCTGGGCTGGGGGTNGGTTGGNNGAGGTCTTTTTTAAAAGGAAGTTACT	1379
	459
GTTATAGAGGGTCTAAGATTCATCCATTTATTTGGCATCTGTTTAAAGTAGATTAGATCC	1439
	479
GAATTC	

SEQ ID NO.3 (SUITE)

FIG.1e

FIG. 2

CCR5	I		II	
	1	M YQVSSPI D I N Y T S E P C Q N I N V K Q I A R L L P P L Y S L V F I F G F V G N M I V I L I N C K R L K S M T D I Y L I N L A I S D I F E I I T		83
		M L S T S R S R F T R N T N E S G E E V T T F E T Y D Y G A P C Q I N F T N K Q I A R L L P P L Y S L V F I F G F V G N M I V I L I N C K R L K S M T D I Y L I N L A I S D I F E I I T		95
		M T T S I F V E T F G T S Y Y D D V G L I E K A D T R A I M A Q F V P P L Y S L V F I F G F V G N M I V I L I N C K R L K S M T D I Y L I N L A I S D I F E I I T		8
		M E T P N T T E D Y D T T F E D Y G D A T P C Q N V E R A F G A Q L L P P L Y S L V F I F G F V G N M I V I L I N C K R L K S M T D I Y L I N L A I S D I F E I I T		92
CCR5	III		IV	
		M N P T D I A D T T L D E S I Y S N Y L Y E S I P K P Q I K E G I K A F G E L R L P P L Y S L V F I F G F V G N M I V I L I N C K R L K S M T D I Y L I N L A I S D I F E I I T		83
		V P F W A H I Y A R A Q W D F G N I M C Q L L T G I Y E I G F F S G I F F T I L L T I D R Y L A M V I A V F A L K A R T V T F G V V T S V I T W V A V F A S L P G I I F I R Q K E G I I		177
		I P L W A H I Y A R A Q W D F G N I M C Q L L T G I Y E I G F F S G I F F T I L L T I D R Y L A M V I A V F A L K A R T V T F G V V T S V I T W V A V F A S L P G I I F I R Q K E G I I		189
		I P F W I Y V R G H R W F C H C M C N L I E C E N M H T G L Y S E I F F T I L L T I D R Y L A M V I A V F A L K A R T V T F G V V T S V I T W V A V F A S L P G I I F I R Q K E G I I		182
CCR5	V		VI	
		I P F W I Y K I K D I W F G D A M C K I I S G E N Y T G L Y S E I F F T I L L T I D R Y L A M V I A V F A L K A R T V T F G V V T S V I T W V A V F A S L P G I I F I R Q K E G I I		182
		I P F W E Y Y A R A Q W D F G N I M C Q L L T G I Y E I G F F S G I F F T I L L T I D R Y L A M V I A V F A L K A R T V T F G V V T S V I T W V A V F A S L P G I I F I R Q K E G I I		186
		Y T C S I I F P P Y S Q Y Q F W K N F Q T L K T V I I G L V I P L I V M V I C Y S G I L K T L L R C R N E K K R H R A V R L I F T I M I V Y F L E W A P Y N I V L L I N T F Q E F F G L N N C		272
		T I I S A I Y E D T V Y S M R H I I F T I R M T I F C I V I P L I V M V I C Y S G I L K T L L R C R N E K K R H R A V R L I F T I M I V Y F L E W A P Y N I V L L I N T F Q E F F G L N N C		280
CCR5	VII		VIII	
		I T C S I I F P P Y S Q Y Q F W K N F Q T L K T V I I G L V I P L I V M V I C Y S G I L K T L L R C R N E K K R H R A V R L I F T I M I V Y F L E W A P Y N I V L L I N T F Q E F F G L N N C		27
		T Y C K P K Y S I N S T T W K V L S S E I N I I G L V I P L I V M V I C Y S G I L K T L L R C R N E K K R H R A V R L I F T I M I V Y F L E W A P Y N I V L L I N T F Q E F F G L N N C		27
		S G S H R I D Q A M Q V T E T L G M T H C C I N P I I Y A F V G E K E R N I I L V F E K K I I T A K R E C K C S I F C Q I E A P E R A S S V Y I I S T G E Q E I S V S I		352
		F F S S Q D Q A I Q V T E T L G M T H C C I N P I I Y A F V G E K E R N I I L V F E K K I I T A K R E C K C P V F E K I I P V D G V T I N I I S T G E Q E N S A I I		360
CCR5	IX		X	
		F E R K H I D V I I V T E V T A Y S H C C E N I V I Y A F V G E K E R N I I L V F E K K I I T A K R E C K C P V F E K I I P V D G V T I N I I S T G E Q E N S A I I		355
		E C E R H I D V I I V T E V T A Y S H C C E N I V I Y A F V G E K E R N I I L V F E K K I I T A K R E C K C P V F E K I I P V D G V T I N I I S T G E Q E N S A I I		355
		T F E R Y L D I A I Q A T E T L A F V H C C I N P I I Y E F G E K E R N I I L V F E K K I I T A K R E C K C P V F E K I I P V D G V T I N I I S T G E Q E N S A I I		360
		T F E R Y L D I A I Q A T E T L A F V H C C I N P I I Y E F G E K E R N I I L V F E K K I I T A K R E C K C P V F E K I I P V D G V T I N I I S T G E Q E N S A I I		360

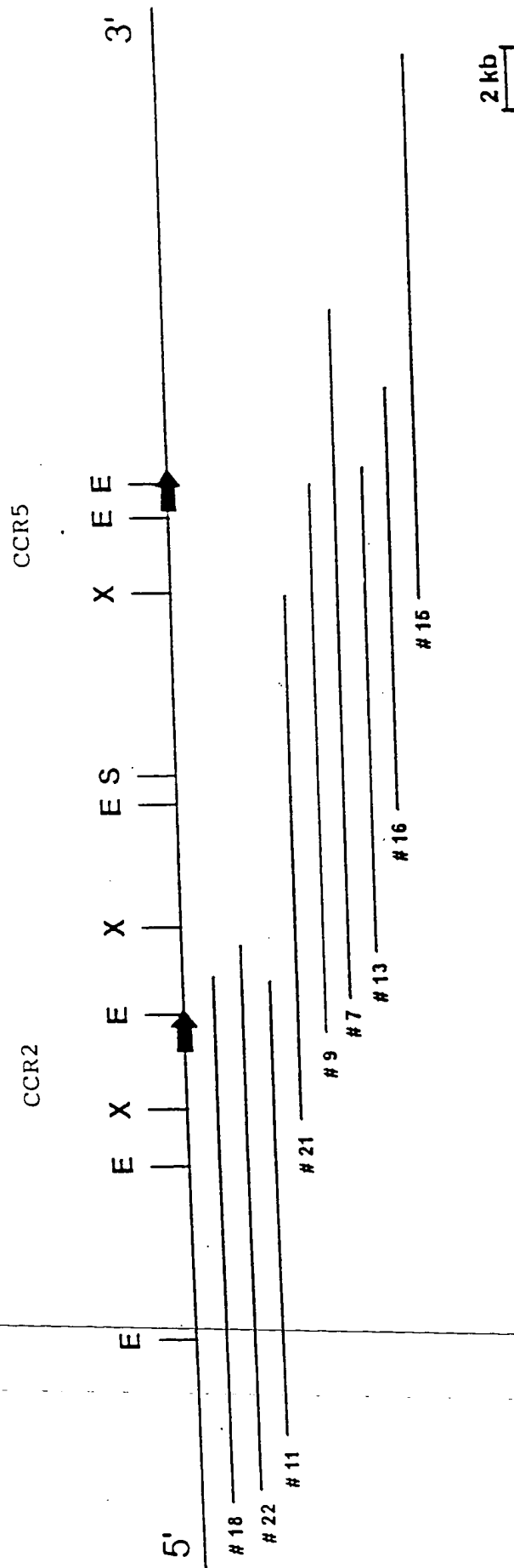


FIG. 3

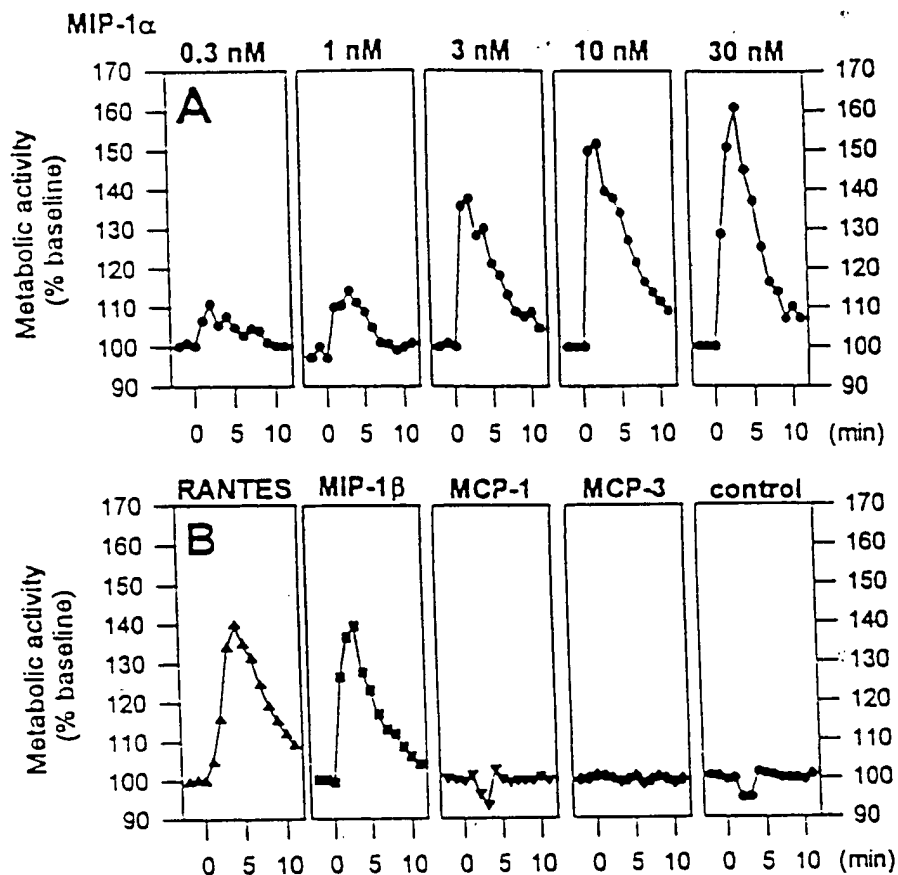


FIG. 4a

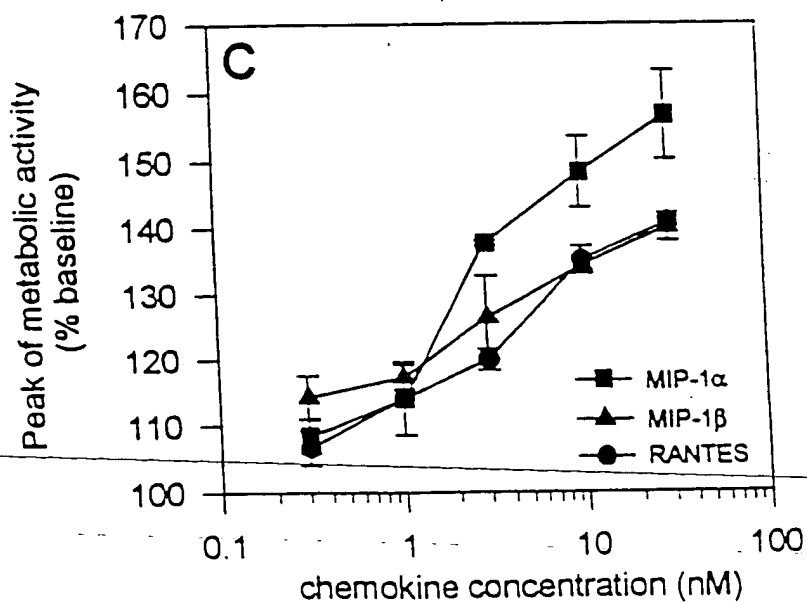


FIG. 4b

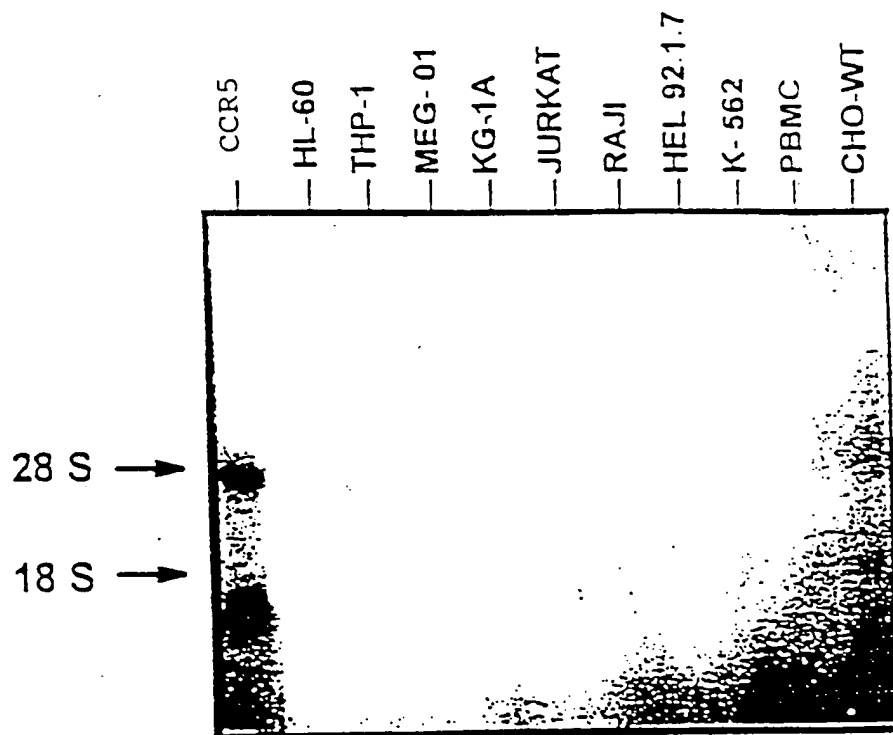


FIG. 5

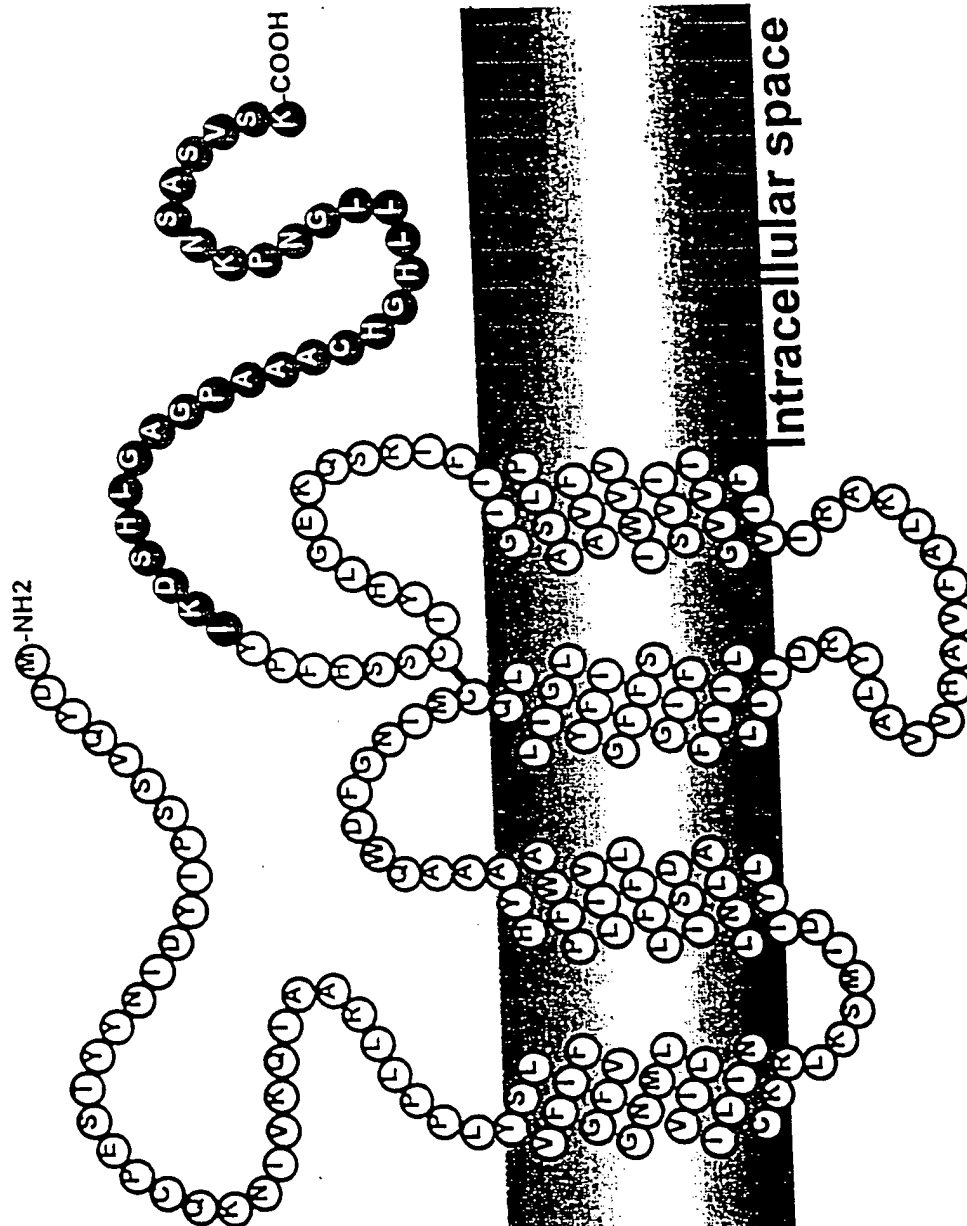
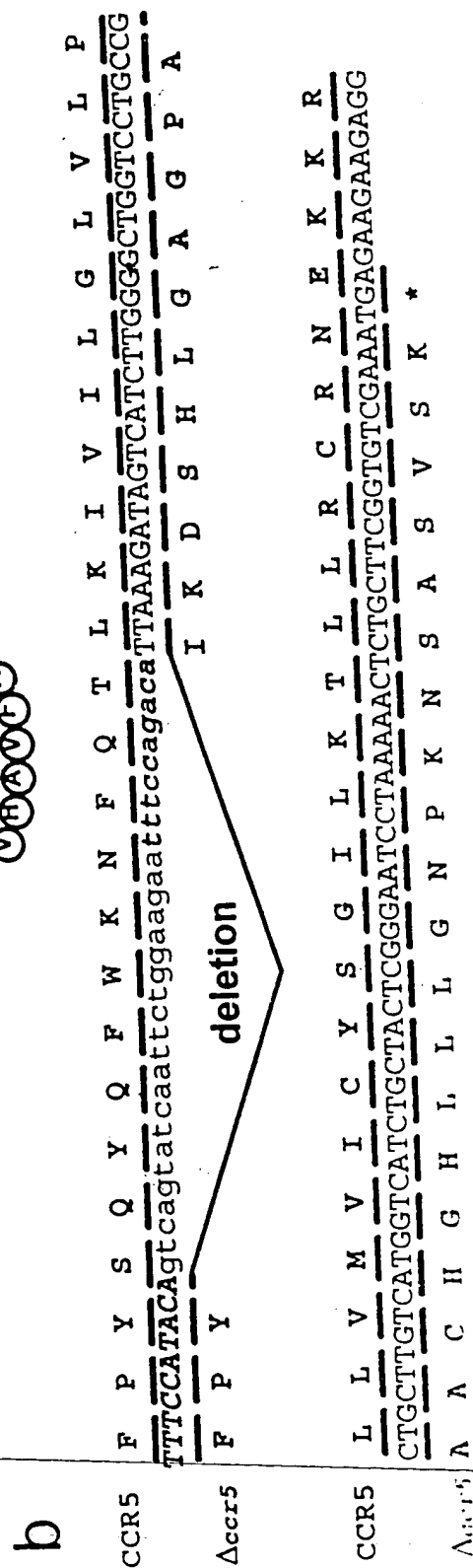


FIG. 6



A.

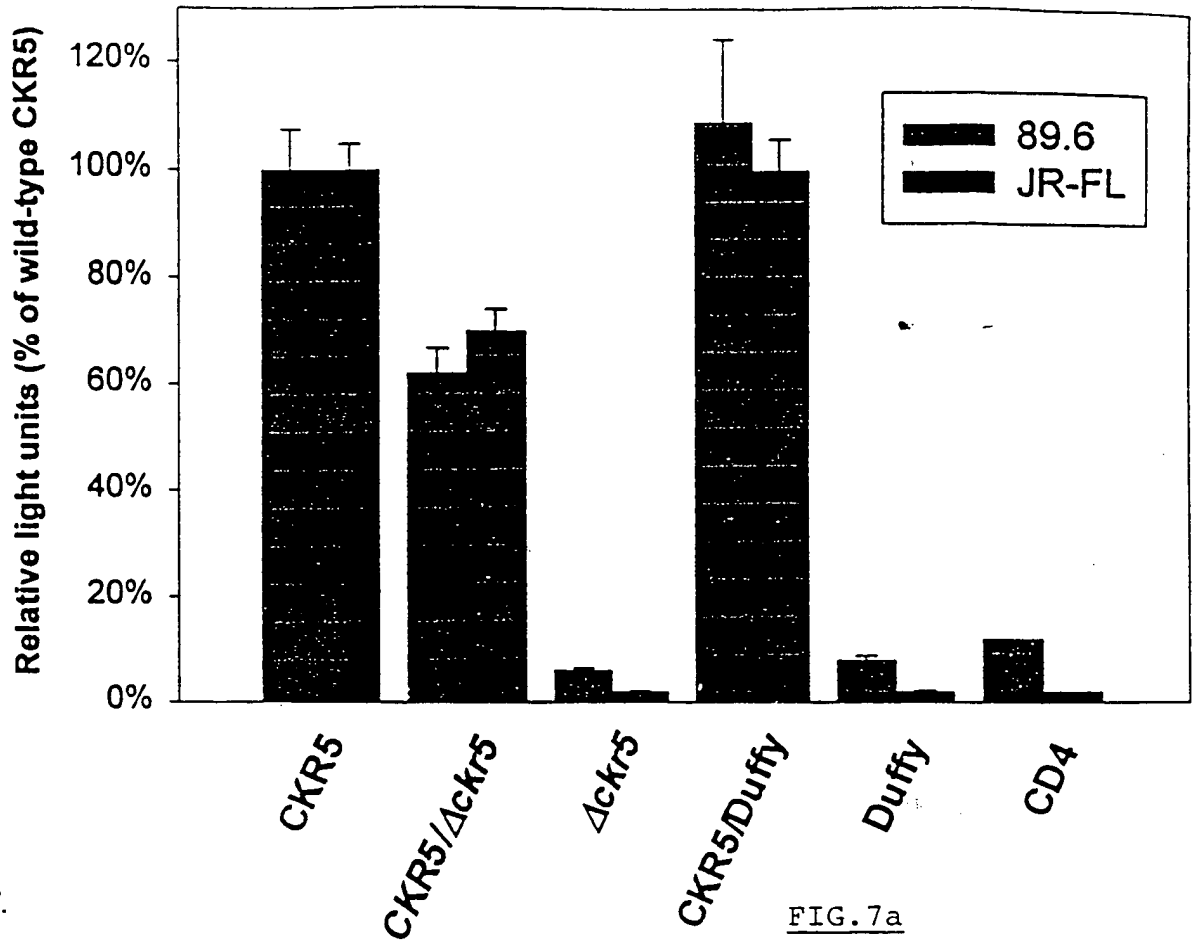


FIG. 7a

B.

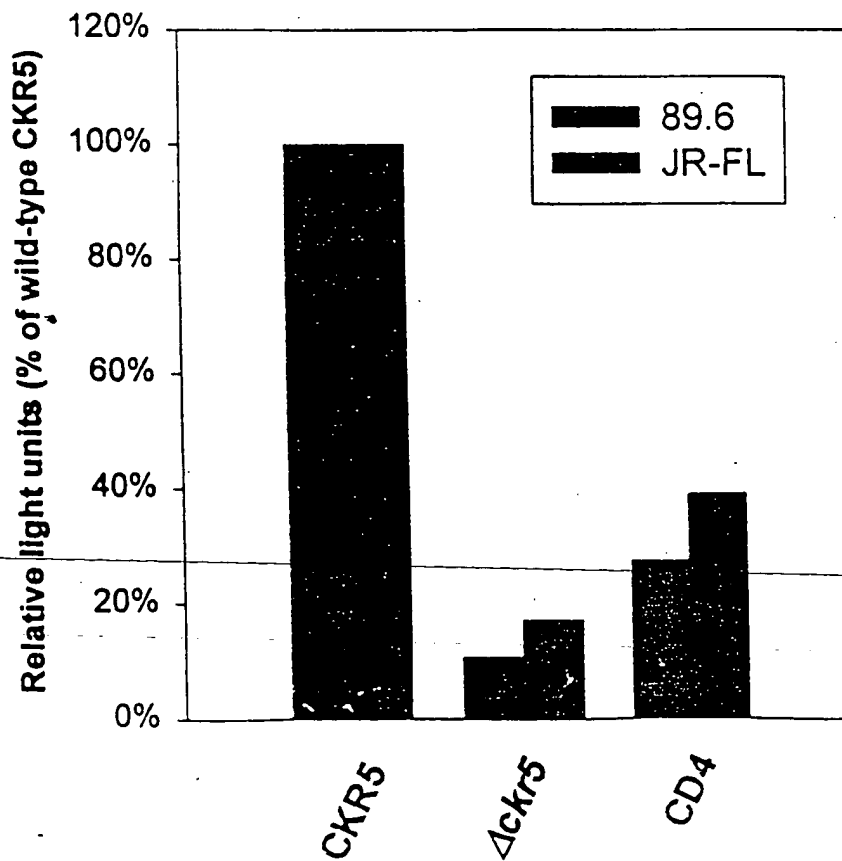


FIG. 7b

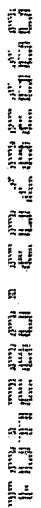


FIG. 8

FORM 22600

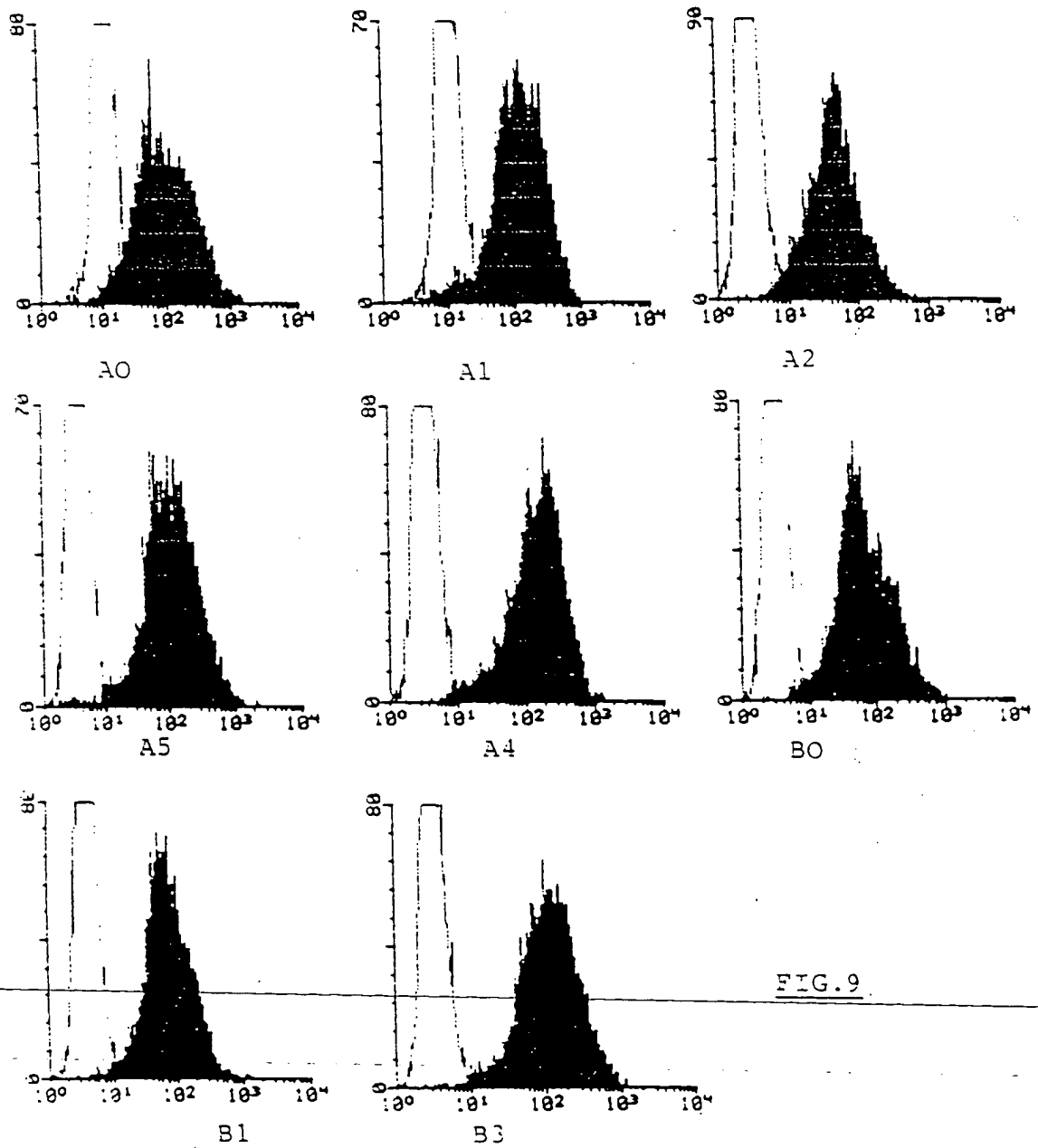


FIG. 9

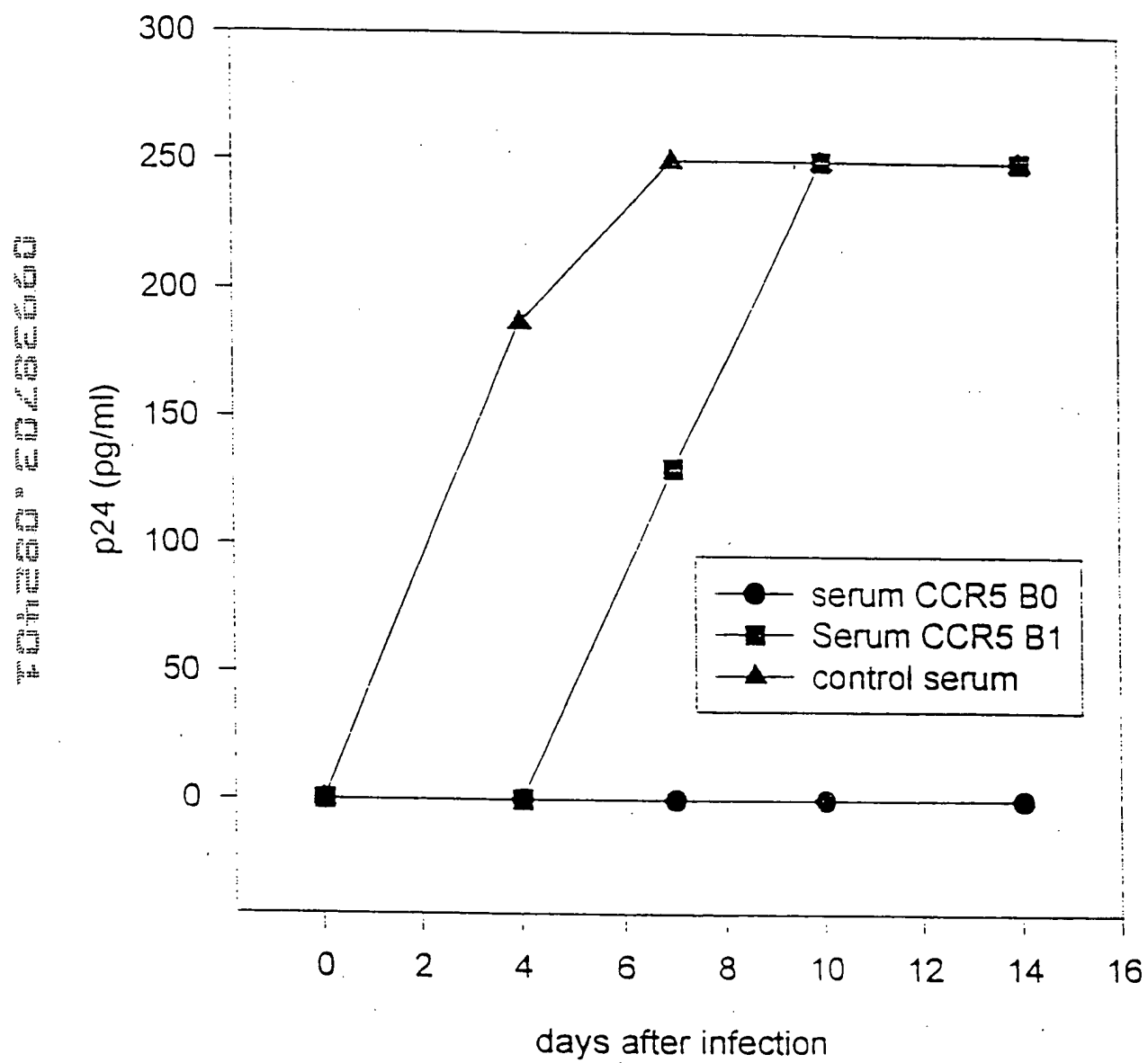


FIG.10